

SEQUENCE LISTING

110> WOLD, WILLIAM TOLLEFSON, ANN

100		,	ANI	•											
<120>	ADENOV TRAIL	VIRUS	REI	PLICA	OITA	1-C01	мретв	ENT V	/ECT(ORS I	EXPRI	ESSIN	1G		
·<130>	INGN:106US														
	10/810,063 2004-03-26														
	60/45														
	> 2003-03-28														
<160> 3															
<170> PatentIn Ver. 2.1															
<210>															
<212>															
<213>	Homo s	sapie	ens												
<220>															
<221>															
<222>	(88).	. (933	3)												
<400> 1 cctcactgac tataaaagaa tagagaagga agggcttcag tgaccggctg cctggctgac 60															
cctca	ctgac 1	tataa	aaaga	aa ta	agaga	aagga	a aqc	agett	caq	tgad	ccaa	cta d	rctac	actgac.	60
			_				-	, ,		- 5	23	5	, , , ,	joojuo	00
ttaca	gcagt (cagac	_	ga ca	aggat		tg go	t at	g at	g ga	ag gt	c ca	ag gg	gg gga	
ttaca	gcagt (cagac	_	ga ca	aggat		tg go	t at	g at	g ga	ag gt	c ca	ag gg	-	
			ctctg			Me	tg go et Al	ct at .a Me	et Me	ig ga	ag gt lu Va 5	ic ca	ag gg ln Gl	gg gga Ly Gly	114
ccc a	gcagt (gc ctg er Leu	gga	cag	acc	tgc	Me gtg	tg go et Al 1 ctg	ct at	et Me	g ga et G	ag gt lu Va 5 ttc	al Gl	ag gg ln Gl	gg gga Ly Gly	
ccc a	gc ctg	gga	cag	acc	tgc	Me gtg	tg go et Al 1 ctg	ct at	et Me	g ga et G	ag gt lu Va 5 ttc	al Gl	ag gg ln Gl	gg gga Ly Gly	114
ccc ag Pro So 10	gc ctg er Leu ag tct	gga Gly ctc	cag Gln tgt	acc Thr 15 gtg	tgc Cys gct	gtg Val gta	tg gcet Al 1 ctg Leu act	atc Ile	gtg Yal 20	atc Ile	ag gt lu Va 5 ttc Phe	aca Thr	ag gg ln Gl gtg Val	gg gga Ly Gly ctc Leu 25	114
ccc ag Pro So 10	gc ctg er Leu	gga Gly ctc	cag Gln tgt Cys	acc Thr 15 gtg	tgc Cys gct	gtg Val gta	tg gcet Al 1 ctg Leu act	atc Ile tac	gtg Yal 20	atc Ile	ag gt lu Va 5 ttc Phe	aca Thr	ag gg ln Gl gtg Val aac Asn	gg gga Ly Gly ctc Leu 25	114
ccc ag Pro So 10 ctg ca Leu G	gc ctg er Leu ag tct ln Ser	gga Gly ctc Leu	cag Gln tgt Cys	acc Thr 15 gtg Val	tgc Cys gct Ala	gtg Val gta Val	tg goet Al 1 ctg Leu act	atc atc Ile tac Tyr 35	gtg Val 20 gtg Val	atc Ile tac	ag gt lu Va 5 ttc Phe ttt	aca Thr	gtg Val aac Asn	gg gga Ly Gly ctc Leu 25 gag Glu	114 162 210
ccc ag Pro So 10 ctg ca Leu G	gc ctg er Leu ag tct ln Ser	gga Gly ctc Leu	cag Gln tgt Cys 30	acc Thr 15 gtg Val	tgc Cys gct Ala	gtg Val gta Val	tg gcet Al l ctg Leu act Thr	atc Ile tac Tyr 35	gtg Val 20 gtg Val	atc Ile tac Tyr	ag gt lu Va 5 ttc Phe ttt Phe	aca Thr	gtg Val aac Asn 40	gg gga Ly Gly ctc Leu 25 gag Glu	114
ccc ag Pro So 10 ctg ca Leu G	gc ctg er Leu ag tct ln Ser	gga Gly ctc Leu	cag Gln tgt Cys 30	acc Thr 15 gtg Val	tgc Cys gct Ala	gtg Val gta Val	tg gcet Al l ctg Leu act Thr	atc Ile tac Tyr 35	gtg Val 20 gtg Val	atc Ile tac Tyr	ag gt lu Va 5 ttc Phe ttt Phe	aca Thr	gtg Val aac Asn 40	gg gga Ly Gly ctc Leu 25 gag Glu	114 162 210
ccc ag Pro So 10 ctg cc Leu G	gc ctg er Leu ag tct ln Ser ag cag ys Gln	gga Gly ctc Leu atg Met 45	cag Gln tgt Cys 30 cag Gln	acc Thr 15 gtg Val gac Asp	tgc Cys gct Ala aag Lys	gtg Val gta Val tac	tg goet Al ctg Leu act Thr tcc Ser 50	atc Ile tac Tyr 35 aaa Lys	gtg Val 20 gtg Val agt Ser	atc Ile tac Tyr	ag gt lu Va 5 ttc Phe ttt Phe	aca Thr acc Thr gct Ala	gtg Val aac Asn 40	gg gga Ly Gly ctc Leu 25 gag Glu ttc Phe	114 162 210
ccc ag Pro So 10 ctg cc Leu G	gc ctg er Leu ag tct ln Ser ag cag ys Gln aa gaa ys Glu	gga Gly ctc Leu atg Met 45	cag Gln tgt Cys 30 cag Gln	acc Thr 15 gtg Val gac Asp	tgc Cys gct Ala aag Lys	gtg Val gta Val tac Tyr	tg goet Al l ctg Leu act Thr tcc Ser 50 gac	atc Ile tac Tyr 35 aaa Lys	gtg Val 20 gtg Val agt Ser	atc Ile tac Tyr ggc Gly	ag gt lu Va 5 ttc Phe ttt Phe att Ile	aca Thr acc Thr gct Ala 55	gtg Val aac Asn 40 tgt Cys	gg gga Ly Gly ctc Leu 25 gag Glu ttc Phe	114 162 210 258
ccc ag Pro So 10 ctg cc Leu G	gc ctg er Leu ag tct ln Ser ag cag ys Gln aa gaa	gga Gly ctc Leu atg Met 45	cag Gln tgt Cys 30 cag Gln	acc Thr 15 gtg Val gac Asp	tgc Cys gct Ala aag Lys	gtg Val gta Val tac Tyr	tg goet Al l ctg Leu act Thr tcc Ser 50 gac	atc Ile tac Tyr 35 aaa Lys	gtg Val 20 gtg Val agt Ser	atc Ile tac Tyr ggc Gly	ag gt lu Va 5 ttc Phe ttt Phe	aca Thr acc Thr gct Ala 55	gtg Val aac Asn 40 tgt Cys	gg gga Ly Gly ctc Leu 25 gag Glu ttc Phe	114 162 210 258
ccc as Pro Sc 10 ctg ca Leu G	gc ctg er Leu ag tct ln Ser ag cag ys Gln aa gaa ys Glu 60 gc ccc	gga Gly ctc Leu atg Met 45 gat Asp	cag Gln tgt Cys 30 cag Gln gac Asp	acc Thr 15 gtg Val gac Asp	tgc Cys gct Ala aag Lys tat Tyr	gtg Val gta Val tac Tyr tgg Trp 65	tg goet Al ctg Leu act Thr tcc Ser 50 gac Asp	atc Ile tac Tyr 35 aaa Lys ccc Pro	gtg Val 20 Val agt Ser aat Asn	atc Ile tac Tyr ggc Gly gac Asp	ag gtlu Va ttc Phe ttt Phe att Ile gaa Glu 70 cag	aca Thr acc Thr gct Ala 55 gag Glu	gtg Val aac Asn 40 tgt Cys agt Ser	gg gga Ly Gly ctc Leu 25 gag Glu ttc Phe atg Met	114 162 210 258
ccc as Pro Sc 10 ctg ca Leu G	gc ctg er Leu ag tct ln Ser ag cag ys Gln aa gaa ys Glu 60 gc ccc er Pro	gga Gly ctc Leu atg Met 45 gat Asp	cag Gln tgt Cys 30 cag Gln gac Asp	acc Thr 15 gtg Val gac Asp	tgc Cys gct Ala aag Lys tat Tyr	gtg Val gta Val tac Tyr tgg Trp 65	tg goet Al ctg Leu act Thr tcc Ser 50 gac Asp	atc Ile tac Tyr 35 aaa Lys ccc Pro	gtg Val 20 Val agt Ser aat Asn	atc Ile tac Tyr ggc Gly gac Asp cgt Arg	ag gtlu Va ttc Phe ttt Phe att Ile gaa Glu 70 cag	aca Thr acc Thr gct Ala 55 gag Glu	gtg Val aac Asn 40 tgt Cys agt Ser	gg gga Ly Gly ctc Leu 25 gag Glu ttc Phe atg Met	114 162 210 258
ccc as Pro Sc 10 ctg ca Leu G	gc ctg er Leu ag tct ln Ser ag cag ys Gln aa gaa ys Glu 60 gc ccc	gga Gly ctc Leu atg Met 45 gat Asp	cag Gln tgt Cys 30 cag Gln gac Asp	acc Thr 15 gtg Val gac Asp	tgc Cys gct Ala aag Lys tat Tyr	gtg Val gta Val tac Tyr tgg Trp 65	tg goet Al ctg Leu act Thr tcc Ser 50 gac Asp	atc Ile tac Tyr 35 aaa Lys ccc Pro	gtg Val 20 Val agt Ser aat Asn	atc Ile tac Tyr ggc Gly gac Asp	ag gtlu Va ttc Phe ttt Phe att Ile gaa Glu 70 cag	aca Thr acc Thr gct Ala 55 gag Glu	gtg Val aac Asn 40 tgt Cys agt Ser	gg gga Ly Gly ctc Leu 25 gag Glu ttc Phe atg Met	114 162 210 258

Lys 90	Met	Ile	Leu	Arg	Thr 95	Ser	Glu	Glu	Thr	Ile 100	Ser	Thr	Val	Gln	Glu 105	
									_	_	_			cag Gln 120		450
gta Val	_	_						_		_	_			ttg Leu		498
				_		_	_	_	_		_			aac Asn		546
	_				_						_		-	cac His		594
			_	_	_			_						atc Ile		642
					-		_		_			_		aca Thr 200	_	690
	_			_	-									tat Tyr		738
														tct Ser		786
_	_	_												ttt Phe		834
														cac His		882
														gtt Val 280		930
taa ctgacctgga aagaaaaagc aataacctca aagtgactat tcagttttca												983				
gga	gata	aca d	ctato	gaaga	at gt	ttca	aaaa	a ato	ctgad	ccaa	aaca	aaaca	aaa (cagaa	aaacag	1043
aaaacaaaaa aacctctatg caatctgagt agagcagcca caaccaaaaa attctacaac												1103				
acacactgtt ctgaaagtga ctcacttatc ccaagaaaat gaaattgctg aaagatcttt											1163					
caggactcta cctcatatca gtttgctagc agaaatctag aagactgtca gcttccaaac											1223					

attaatgcaa tggttaacat cttctgtctt tataatctac tccttgtaaa gactgtagaa 1283
gaaagcgcaa caatccatct ctcaagtagt gtatcacagt agtagcctcc aggtttcctt 1343
aagggacaac atccttaagt caaaagagag aagaggcacc actaaaagat cgcagtttgc 1403
ctggtgcagt ggctcacacc tgtaatccca acattttggg aacccaaggt gggtagatca 1463
cgagatcaag agatcaagac catagtgacc aacatagtga aaccccatct ctactgaaag 1523
tgcaaaaatt agctgggtgt gttggcacat gcctgtagtc ccagctactt gagaggctga 1583
ggcaggagaa tcgtttgaac ccgggaggca gaggttgcag tgtggtgaga tcatgccact 1643
acactccagc ctggcgacag agcgagactt ggtttcaaaa aaaaaaaaa aaaaaaactt 1703
cagtaagtac gtgttattt tttcaataaa attctattac agtatgcaa aaaaaaaaa 1763
aaaaaa

<210> 2

<211> 281

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val 70 75 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro 105 100 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly 120 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu 135 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly 150 155 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile 170 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe 185 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln 200 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys 215 220 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr

<210> 3
<211> 14
<212> DNA
<213> Artificial Sequence
<220>
<221> modified_base
<222> (3)..(12)
<223> n = a, c, g and/or t/u
<220>
<223> Description of Artifical

<223> Description of Artificial Sequence: Synthetic Primer

<400> 3 ctngaanntt cnag